

SEQUENCE LISTING

<110> Tsukahara, Kappei
 Tsuchiya, Mamiko
 Jigami, Yoshifumi
 Nakayama, Kenichi
 Umemura, Mariko
 Okamoto, Michiyo

<120> METHOD OF SCREENING FOR COMPOUNDS THAT
 INHIBIT THE ENZYMATIC ACTIVITY OF GWT1 GENE PRODUCT

<130> 082368-004400US

<140> 10/536,935

<141> 2006-02-15

<150> PCT/JP03/14909

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Phe Gln Tyr His Pro Tyr Ser Val Ser Arg Arg Phe Ala Asn Leu Pro	
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Cys Leu Thr Asp Lys Ile Phe Gly Asn Ser Ser Glu Tyr Tyr Lys Val	
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gcc gaa tgc ttg gaa tca atc aac tcc aat ggg ttg ttt tta ttt ttg	1344
Ala Glu Cys Leu Glu Ser Ile Asn Ser Asn Gly Leu Phe Leu Phe Leu	
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 85 90 95
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180 185 190	
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      20              25              30

tca tct tat ttg tcc ttt aga ttg ttg aaa aag tct ctt ggt gat tta      144
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gct ttg att tac gac tac att ctt aat gtg ttg aca att cta gca tcc      192
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Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro
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tct tca ccc cat aga caa aat gat aca aaa gaa gat aaa tcg gac gaa      336
Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu
      100             105             110

cta ttg ccg aga aaa caa ttt ata aca gcc tat cgt tct caa atg ttg      384
Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu
      115             120             125

ata att act aat cta gct ata tta gct gtt gat ttt cct att ttc cca      432
Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro
      130             135             140

aga aga ttt gcc aaa gtg gaa aca tgg ggc acg tca atg atg gat tta      480
Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu
      145             150             155             160

gga gtt ggg tcg ttt gtg ttc tcc atg ggg ttg gct aat tct cga caa      528
Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln
      165             170             175

ttg atc aag aac cac acc gac aat tac aaa ttt agt tgg aag agt tat      576
Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr
      180             185             190

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tta gga gct att cgt ttt gtt agt gtt aag caa ttg gac tat cag gaa Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu 210 215 220	672
cac gaa aca gag tat gga atc cat tgg aat ttt ttc ttc aca tta ggg His Glu Thr Glu Tyr Gly Ile His Trp Asn Phe Phe Phe Thr Leu Gly 225 230 235 240	720
ttc ttg cca att gta ttg gga ata tta gac ccg gtg ttg aat ttg gtt Phe Leu Pro Ile Val Leu Gly Ile Leu Asp Pro Val Leu Asn Leu Val 245 250 255	768
cca cgc ttc ata ata gga att ggt atc tca att ggt tat gag gta gcg Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Gly Tyr Glu Val Ala 260 265 270	816
ttg aat aag act ggt ttg ttg aag ttc att ttg agc agc gaa aac aga Leu Asn Lys Thr Gly Leu Leu Lys Phe Ile Leu Ser Ser Glu Asn Arg 275 280 285	864
ctt gaa tct ctc atc gcc atg aat aaa gaa ggt att ttt tcg ttt att Leu Glu Ser Leu Ile Ala Met Asn Lys Glu Gly Ile Phe Ser Phe Ile 290 295 300	912
gga tat ctt tgt att ttt ata att ggt cag tct ttt ggg tca ttt gtt Gly Tyr Leu Cys Ile Phe Ile Ile Gly Gln Ser Phe Gly Ser Phe Val 305 310 315 320	960
tta aca ggc tac aaa aca aag aac aac tta ata acc att agc aaa att Leu Thr Gly Tyr Lys Thr Lys Asn Asn Leu Ile Thr Ile Ser Lys Ile 325 330 335	1008
cgt att tca aaa aaa caa cac aag aaa gag ctg ctg ctg ttt ttc tca Arg Ile Ser Lys Lys Gln His Lys Lys Glu Leu Leu Leu Phe Phe Ser 340 345 350	1056
gtc gcc act act cag gga tta tat ttg gca tgt atc ttc tat cac tta Val Ala Thr Thr Gln Gly Leu Tyr Leu Ala Cys Ile Phe Tyr His Leu 355 360 365	1104
gct ttc agt ttg ttc atc agc aac tta tca ttc ttg caa cca att tca Ala Phe Ser Leu Phe Ile Ser Asn Leu Ser Phe Leu Gln Pro Ile Ser 370 375 380	1152
aga cga ttg gcc aat ttc ccc tac gtc atg tgg gtc gtt tcg tac aat Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn 385 390 395 400	1200

gct acg ttt tta tta tgt tat gac tta att gaa aaa ttt atc ccg ggg 1248
 Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly
 405 410 415

aac ctt act tct act gta ttg gac tct att aat aac aat ggt tta ttt 1296
 Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe
 420 425 430

atc ttc ttg gtc agc aat tta tta aca ggg ttt att aac atg tcc atc 1344
 Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile
 435 440 445

aac act ttg gaa act agc aat aaa atg gca gtg att atc ttg att ggc 1392
 Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly
 450 455 460

tat agt ctt act tgg aca ttg ctc gcc tta tat ttg gat aag agg aag 1440
 Tyr Ser Leu Thr Trp Thr Leu Leu Ala Leu Tyr Leu Asp Lys Arg Lys
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 35 40 45

Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser
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Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val
 65 70 75 80

Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro
 85 90 95

Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu
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 Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu
 115 120 125
 Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro
 130 135 140
 Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu
 145 150 155 160
 Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln
 165 170 175
 Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr
 180 185 190
 Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val
 195 200 205
 Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu
 210 215 220
 His Glu Thr Glu Tyr Gly Ile His Trp Asn Phe Phe Phe Thr Leu Gly
 225 230 235 240
 Phe Leu Pro Ile Val Leu Gly Ile Leu Asp Pro Val Leu Asn Leu Val
 245 250 255
 Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Gly Tyr Glu Val Ala
 260 265 270
 Leu Asn Lys Thr Gly Leu Leu Lys Phe Ile Leu Ser Ser Glu Asn Arg
 275 280 285
 Leu Glu Ser Leu Ile Ala Met Asn Lys Glu Gly Ile Phe Ser Phe Ile
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 Gly Tyr Leu Cys Ile Phe Ile Ile Gly Gln Ser Phe Gly Ser Phe Val
 305 310 315 320
 Leu Thr Gly Tyr Lys Thr Lys Asn Asn Leu Ile Thr Ile Ser Lys Ile
 325 330 335
 Arg Ile Ser Lys Lys Gln His Lys Lys Glu Leu Leu Leu Phe Phe Ser
 340 345 350
 Val Ala Thr Thr Gln Gly Leu Tyr Leu Ala Cys Ile Phe Tyr His Leu
 355 360 365

Ala Phe Ser Leu Phe Ile Ser Asn Leu Ser Phe Leu Gln Pro Ile Ser
370 375 380

Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn
385 390 395 400

Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly
405 410 415

Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe
420 425 430

Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile
435 440 445

Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly
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Ile Tyr Ile Lys Leu
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tca agt tcc att gag aca tgt ggc ttg tta tta ata gga att gct tgc 96
Ser Ser Ser Ile Glu Thr Cys Gly Leu Leu Leu Ile Gly Ile Ala Cys
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aac gtt ttg tgg gta aac atg act gcg aga aac atc tta ccc aaa ggg 144
Asn Val Leu Trp Val Asn Met Thr Ala Arg Asn Ile Leu Pro Lys Gly
35 40 45

aat ctt ggg ttt ctt gtt gag ttt ttc atc ttt tgc tta att cca tta 192
Asn Leu Gly Phe Leu Val Glu Phe Phe Ile Phe Cys Leu Ile Pro Leu
50 55 60

ttt gtc att tac gtt tca tgc aaa gtt ggc gtt ttc act ctt tgc ata	240
Phe Val Ile Tyr Val Ser Ser Lys Val Gly Val Phe Thr Leu Cys Ile	
65 70 75 80	
gcc tct ttt ttg cct tcc ttc gtc ctt cat gtt ata agt cca att aat	288
Ala Ser Phe Leu Pro Ser Phe Val Leu His Val Ile Ser Pro Ile Asn	
85 90 95	
tgg gat gtg ctg aga aga aaa cct ggt tgt tgt ctt act aaa aaa aat	336
Trp Asp Val Leu Arg Arg Lys Pro Gly Cys Cys Leu Thr Lys Lys Asn	
100 105 110	
gaa aat act ttt gat cga cga att gct gga gtc aca ttt tat cgt tct	384
Glu Asn Thr Phe Asp Arg Arg Ile Ala Gly Val Thr Phe Tyr Arg Ser	
115 120 125	
caa atg atg ttg gtt act gtc act tgc atc ctg gcc gtt gac ttt acc	432
Gln Met Met Leu Val Thr Val Thr Cys Ile Leu Ala Val Asp Phe Thr	
130 135 140	
ctt ttc ccg agg aga tat gcc aaa gtt gaa acc tgg gga aca tca ctg	480
Leu Phe Pro Arg Arg Tyr Ala Lys Val Glu Thr Trp Gly Thr Ser Leu	
145 150 155 160	
atg gat ctt ggt gtt gga tct ttc atg ttt tct tca ggt act gtg got	528
Met Asp Leu Gly Val Gly Ser Phe Met Phe Ser Ser Gly Thr Val Ala	
165 170 175	
gga cgg aaa aat gac att aaa aaa cca aat gcg ttt aaa aat gta ttg	576
Gly Arg Lys Asn Asp Ile Lys Lys Pro Asn Ala Phe Lys Asn Val Leu	
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tgg aat tct ttc atc ctt ttg att tta gga ttt gcg cgc atg ttt tta	624
Trp Asn Ser Phe Ile Leu Leu Ile Leu Gly Phe Ala Arg Met Phe Leu	
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acg aaa agc atc aat tac caa gaa cat gta agc gaa tat ggc atg cat	672
Thr Lys Ser Ile Asn Tyr Gln Glu His Val Ser Glu Tyr Gly Met His	
210 215 220	
tgg aac ttt ttt ttc acc cta ggt ttc atg gct ctt ggc gta ttt ttt	720
Trp Asn Phe Phe Phe Thr Leu Gly Phe Met Ala Leu Gly Val Phe Phe	
225 230 235 240	
ttt cgt cgt tct tta aaa aaa gtc tcc tat ttt aat tta gca acc ttc	768
Phe Arg Arg Ser Leu Lys Lys Val Ser Tyr Phe Asn Leu Ala Thr Phe	
245 250 255	
att act ctt ctt cat cat tgt ttg ctt gtt tta acc cct ttc caa aaa	816
Ile Thr Leu Leu His His Cys Leu Leu Val Leu Thr Pro Phe Gln Lys	
260 265 270	

tg	g	c	t	a	t	c	c	c	a	a	a	a	t	t	t	g	c	a	a	a	g		864
Trp	Ala	Leu	Ser	Ala	Pro	Arg	Thr	Asn	Ile	Leu	Ala	Gln	Asn	Arg	Glu								
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g	g	t	a	t	t	c	t	c	c	c	g	a	t	a	c	t	t	t	t	a	t	g	912
Gly	Ile	Ala	Ser	Leu	Pro	Gly	Tyr	Ile	Ala	Ile	Tyr	Phe	Tyr	Gly	Met								
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Tyr	Thr	Gly	Ser	Val	Leu	Ala	Asp	Arg	Pro	Leu	Met	Tyr	Thr	Arg									
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g	c	a	t	a	c	c	a	c	a	t	t	a	t	c	c	a	t	a	c	a	t		1008
Ala	Glu	Ser	Trp	Lys	Arg	Phe	Gln	Arg	Leu	Leu	Phe	Pro	Leu	Cys	Ile								
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t	t	a	t	a	c	c	a	c	a	t	t	a	t	c	a	t	a	c	a	t			1056
Leu	Leu	Val	Leu	Tyr	Leu	Val	Ser	Asn	Phe	Leu	Ser	Val	Gly	Val	Ser								
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c	c	a	c	c	a	c	c	a	c	a	c	a	c	a	c	a	c	a	c	a	c		1104
Arg	Arg	Leu	Ala	Asn	Thr	Pro	Tyr	Val	Ala	Asn	Val	Ala	Phe	Ile	Asn								
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a	t	a	c	a	c	a	c	a	c	a	c	a	c	a	c	a	c	a	c	a	c		1152
Met	Phe	Phe	Leu	Thr	Ile	Tyr	Ile	Leu	Ile	Asp	Ala	Tyr	Leu	Phe	Pro								
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t	c	t	c	t	a	t	a	c	c	a	a	a	c	t	a	c	a	c	a	c			1200
Ser	Ser	Val	Pro	Tyr	Gly	Ser	Arg	Val	Pro	Lys	Leu	Leu	Glu	Asp	Ala								
385					390					395				400									
a	a	a	a	c	a	c	a	c	a	c	a	c	a	c	a	c	a	c	a	c			1248
Asn	Asn	Asn	Gly	Leu	Leu	Val	Phe	Leu	Ile	Ala	Asn	Val	Leu	Thr	Gly								
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g	t	a	a	t	a	c	a	c	a	c	a	c	a	c	a	c	a	c	a	c			1296
Val	Val	Asn	Leu	Ser	Phe	Asp	Thr	Leu	His	Ser	Ser	Asn	Ala	Lys	Gly								
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t	t	a	a	c	a	c	a	c	a	c	a	c	a	c	a	c	a	c	a	c			1344
Leu	Thr	Ile	Met	Thr	Met	Tyr	Leu	Phe	Ile	Ile	Cys	Tyr	Met	Ala	His								
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t	g	c	c	a	c	a	c	a	c	a	c	a	c	a	c	a	c	a	c	a			1380
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<213> Schizosaccharomyces pombe

<220>

<223> Protein

<400> 8

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Asn	Val	Leu	Trp	Val	Asn	Met	Thr	Ala	Arg	Asn	Ile	Leu	Pro	Lys	Gly	
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Phe	Val	Ile	Tyr	Val	Ser	Ser	Lys	Val	Gly	Val	Phe	Thr	Leu	Cys	Ile	
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Trp	Asp	Val	Leu	Arg	Arg	Lys	Pro	Gly	Cys	Cys	Leu	Thr	Lys	Lys	Asn	
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Gln	Met	Met	Leu	Val	Thr	Val	Thr	Cys	Ile	Leu	Ala	Val	Asp	Phe	Thr	
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Met	Asp	Leu	Gly	Val	Gly	Ser	Phe	Met	Phe	Ser	Ser	Gly	Thr	Val	Ala	
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Gly	Arg	Lys	Asn	Asp	Ile	Lys	Lys	Pro	Asn	Ala	Phe	Lys	Asn	Val	Leu	
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Trp	Asn	Ser	Phe	Ile	Leu	Leu	Ile	Leu	Gly	Phe	Ala	Arg	Met	Phe	Leu	
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			435				440					445																																								
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Lys Glu Ala Phe Val Ser Gly Leu Ala Gly Gly Ser Ile Leu Glu Ile	
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Asn Ala Val Thr Leu Val Ala Ser Val Ser Val Phe Leu Trp Ser Ile	
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Leu Gln Ser Arg Leu Ser Phe Phe Thr Pro Tyr Ser Ala Ala Ala Leu	
45 50 55	
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Leu Val Asp Phe Leu Leu Asn Val Leu Ala Ile Leu Phe Ala Thr Thr	
60 65 70	
tta tac tct tcg gcg cct ctt ctt ctc aat ctc ctt cta ata tct ccc	294
Leu Tyr Ser Ser Ala Pro Leu Leu Leu Asn Leu Leu Leu Ile Ser Pro	
75 80 85	
gct ctg ctg ata ctc ctc tct acg aaa cgt cct cgg acc ccc gtc aaa	342
Ala Leu Leu Ile Leu Leu Ser Thr Lys Arg Pro Arg Thr Pro Val Lys	
90 95 100	
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Ala Lys Pro Pro Arg Gln Ser Ala Arg Ala Gly Lys Asp Asp Ser Lys	
105 110 115 120	
cat gcg aca gcc ttg cca gag tct cta ccc att cat cca ttt ctc acg	438
His Ala Thr Ala Leu Pro Glu Ser Leu Pro Ile His Pro Phe Leu Thr	
125 130 135	
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Thr Tyr Arg Ala Ala Met Met Val Ile Thr Cys Ile Ala Ile Leu Ala	
140 145 150	
gtg gat ttt cgc att ttt cct cgc cga ttc gcc aag gta gaa aac tgg	534
Val Asp Phe Arg Ile Phe Pro Arg Arg Phe Ala Lys Val Glu Asn Trp	
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Gly Thr Ser Leu Met Asp Leu Gly Val Gly Ser Phe Val Phe Ser Gly	
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Lys Arg Leu Pro Leu Ala Lys Arg Leu Ile Ala Ser Thr Arg His Ser	
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Ile Pro Leu Leu Val Leu Gly Leu Ile Arg Leu Tyr Ser Val Lys Gly	
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Leu Asp Tyr Ala Glu His Val Thr Glu Tyr Gly Val His Trp Asn Phe	
235 240 245	
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Phe Phe Thr Leu Gly Leu Leu Pro Pro Phe Val Glu Val Phe Asp Ala	
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265 270 275 280	
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Val Leu Tyr Gln Val Ala Leu Glu Ser Thr Asp Leu Lys Ser Tyr Ile	
285 290 295	
ctc gtc tcc cct cgt ggg cca agc tta ctg tcc aag aat cgt gaa ggc	966
Leu Val Ser Pro Arg Gly Pro Ser Leu Leu Ser Lys Asn Arg Glu Gly	
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gtc ttc tcc ttc tca ggt tat ctc gcg att ttt ctt gct ggt cgt gcg	1014
Val Phe Ser Phe Ser Gly Tyr Leu Ala Ile Phe Leu Ala Gly Arg Ala	
315 320 325	
atc gcc att ccg ata atc cct cgc gga act tct ttc tca aga agc cca	1062
Ile Gly Ile Arg Ile Ile Pro Arg Gly Thr Ser Phe Ser Arg Ser Pro	
330 335 340	
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Glu Gln Ala Arg Arg Val Leu Ile Ser Leu Gly Val Gln Ala Leu	
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Val Trp Thr Thr Leu Phe Val Leu Asn Ser Thr Tyr Ala Met Gly Tyr	
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Gly Ala Asn Ile Pro Val Ser Arg Arg Leu Ala Asn Met Pro Tyr Val	
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 Ser Glu Ser Glu Arg Val Asp Phe Ala Thr Ser Arg Ile Met Ser Ala
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gcc atc gct gtt ctc att gga tat tca tcc att atc aca ggg gtt gct 1494
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Thr Pro Tyr Ser Ala Ala Ala Leu Leu Val Asp Phe Leu Leu Asn Val
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Gly Val Gln Ala Leu Val Trp Thr Thr Leu Phe Val Leu Asn Ser Thr	
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375 380 385	
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Asn Met Pro Tyr Val Leu Trp Val Ser Ala Phe Asn Thr Ala Gln Leu	
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Phe Val Phe Cys Leu Ile Glu Thr Leu Cys Phe Pro Ala Val His Arg	
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Thr Thr Thr Gln Glu Ser Glu Ser Glu Arg Val Asp Phe Ala Thr Ser	
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Trp Ser Ile Asn Ala Val Ser Leu Val Ala Leu
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ggggttctgt catttggaga cgcttattaa ttgggatcgc ag gcg aca tat gct      210
                                         Ala Thr Tyr Ala
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ctc tgg atc gcc tta tcg ccg tac atc cgt cat gga ctc ctg aac aac      258
Leu Trp Ile Ala Leu Ser Pro Tyr Ile Arg His Gly Leu Leu Asn Asn
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tac ctg atc tgt gtt ctt ccc cta tta ttc ggg gtg acc atc ttc tca      306
Tyr Leu Ile Cys Val Leu Pro Leu Leu Phe Gly Val Thr Ile Phe Ser
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Thr Ser Pro Leu Val Phe Thr Ser Phe Leu Ser Ile Ile Ser Leu Ala
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Phe Ile Thr Lys Ser Gln Lys Cys Phe Lys Ser Val Ser Ser Pro Glu
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Lys Pro Lys Gly Gln Trp Leu Asp Glu Ser Asp Ser Asp Glu Glu Pro
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gcg gaa cct gct tct gca gct gga tct gca gca gtc tca cca gta aag      498
Ala Glu Pro Ala Ser Ala Ala Gly Ser Ala Ala Val Ser Pro Val Lys
          120          125          130

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His	Glu	Asp	Pro	Leu	Gly	Ile	Met	Gly	Val	Asn	Arg	Arg	Arg	Arg	Ser	Leu													
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Leu	Glu	Gly	Val	Ser	Leu	Asp	Val	Pro	Ser	His	Ile	Asp	Ser	Lys	Val														
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Lys	Ala	Gln	Trp	Val	Lys	Glu	Lys	Gly	Arg	Leu	Pro	Phe	Leu	Thr	Val														
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Tyr	Arg	Ala	His	Met	Met	Leu	Met	Thr	Val	Ile	Cys	Ile	Leu	Ala	Val														
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Asp	Phe	Glu	Val	Phe	Pro	Arg	Trp	Gln	Gly	Lys	Cys	Glu	Asp	Phe	Gly														
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Thr	Ser	Leu																											
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Ser	Ser	Pro	Ala	Leu	Asn	Ser	His	Ile	Ile	Pro	Leu	Thr	Pro	Ser	Pro														
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Phe	Thr	Ser	Ile	Leu	Ile	Ser	Leu	Arg	Lys	Ser	Ile	Pro	Ile	Leu	Val														
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Ser Pro Glu Lys Pro Lys Gly Gln Trp Leu Asp Glu Ser Asp Ser Asp	
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Asp Phe Gly Thr Ser Leu Met Asp Val Gly Val Gly Ser Phe Val Phe	
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tcc ctc ggt ctc gtc tcc aca aaa tct ctt tct cct cca cct cca act	864

Ser	Leu	Gly	Leu	Val	Ser	Thr	Lys	Ser	Leu	Ser	Pro	Pro	Pro	Thr		
		275					280					285				
cct	acg	ccc	tcc	tcg	ccc	gct	ctc	aac	tct	cac	atc	att	ccc	ctc	acc	912
Pro	Thr	Pro	Ser	Ser	Pro	Ala	Leu	Asn	Ser	His	Ile	Ile	Pro	Leu	Thr	
		290				295					300					
cgc	tcc	ccg	ttc	act	tcc	atc	ctc	atc	tcg	ctc	cga	aaa	tcc	atc	ccc	960
Pro	Ser	Pro	Phe	Thr	Ser	Ile	Leu	Ile	Ser	Leu	Arg	Lys	Ser	Ile	Pro	
		305			310					315					320	
atc	ctc	gtc	ctc	ggc	ttt	ata	cgg	ttg	att	atg	gtc	aag	gga	tct	gat	1008
Ile	Leu	Val	Leu	Gly	Phe	Ile	Arg	Leu	Ile	Met	Val	Lys	Gly	Ser	Asp	
				325					330					335		
tat	cct	gag	cat	gtg	acg	gag	tac	ggc	gtg	cac	tgg	aat	ttc	ttc	ttc	1056
Tyr	Pro	Glu	His	Val	Thr	Glu	Tyr	Gly	Val	His	Trp	Asn	Phe	Phe	Phe	
			340					345					350			
acc	ctc	gca	ttg	gtt	cct	gtg	ctc	gcc	gtg	ggc	att	cga	cca	ttg	acg	1104
Thr	Leu	Ala	Leu	Val	Pro	Val	Leu	Ala	Val	Gly	Ile	Arg	Pro	Leu	Thr	
		355					360					365				
cag	tgg	ctt	cgc	tgg	agt	gtg	ctt	ggg	gta	atc	atc	tct	ttg	ctg	cat	1152
Gln	Trp	Leu	Arg	Trp	Ser	Val	Leu	Gly	Val	Ile	Ile	Ser	Leu	Leu	His	
		370			375						380					
cag	ctg	tgg	tta	aca	tat	tat	ctc	caa	tcc	atc	gtc	ttc	tca	ttc	ggc	1200
Gln	Leu	Trp	Leu	Thr	Tyr	Tyr	Leu	Gln	Ser	Ile	Val	Phe	Ser	Phe	Gly	
		385			390					395					400	
cgg	tca	ggc	atc	ttt	cta	gca	aac	aag	gaa	ggc	ttc	tcc	tct	ctt	cct	1248
Arg	Ser	Gly	Ile	Phe	Leu	Ala	Asn	Lys	Glu	Gly	Phe	Ser	Ser	Leu	Pro	
			405					410						415		
ggc	tat	ctt	tcc	ata	ttt	ttg	atc	ggc	ttg	tct	att	gga	gat	cat	gtt	1296
Gly	Tyr	Leu	Ser	Ile	Phe	Leu	Ile	Gly	Leu	Ser	Ile	Gly	Asp	His	Val	
		420					425					430				
tta	agg	ctc	agt	tta	cca	cca	aga	aga	gag	agg	gtc	gtg	tca	gaa	aca	1344
Leu	Arg	Leu	Ser	Leu	Pro	Pro	Arg	Arg	Glu	Arg	Val	Val	Ser	Glu	Thr	
		435					440					445				
aat	gaa	gag	cat	gag	cag	agt	cat	ttt	gag	aga	aaa	aaa	ttg	gat	ttg	1392
Asn	Glu	Glu	His	Glu	Gln	Ser	His	Phe	Glu	Arg	Lys	Lys	Leu	Asp	Leu	
		450			455						460					
att	atg	gag	ttg	att	gga	tat	agc	tta	ggc	tgg	tgg	gca	ctc	tta	gga	1440
Ile	Met	Glu	Leu	Ile	Gly	Tyr	Ser	Leu	Gly	Trp	Trp	Ala	Leu	Leu	Gly	
		465			470					475					480	

ggc tgg att tgg gcc ggc ggg gag gta tcc agg cgt tta gcc aac gct 1488
 Gly Trp Ile Trp Ala Gly Gly Glu Val Ser Arg Arg Leu Ala Asn Ala
 485 490 495

 cct tat gta ttt tgg gta gcg gca tac aat acc acc ttt ctc ctc ggc 1536
 Pro Tyr Val Phe Trp Val Ala Ala Tyr Asn Thr Thr Phe Leu Leu Gly
 500 505 510

 tac ctc ctc ctt acc cac att att cca tct ccc acc tct tcc caa aca 1584
 Tyr Leu Leu Leu Thr His Ile Ile Pro Ser Pro Thr Ser Ser Gln Thr
 515 520 525

 tca cca tcg atc tta gtg cct ccc ttg ctc gac gct atg aat aaa aac 1632
 Ser Pro Ser Ile Leu Val Pro Pro Leu Leu Asp Ala Met Asn Lys Asn
 530 535 540

 ggt ctc gcg ata ttt ttg gcg gcc aac ttg ctt aca gga ctg gtg aat 1680
 Gly Leu Ala Ile Phe Leu Ala Ala Asn Leu Leu Thr Gly Leu Val Asn
 545 550 555 560

 gtg agc atg aag aca atg tat gcg ccg gcg tgg ttg tca atg ggg gtg 1728
 Val Ser Met Lys Thr Met Tyr Ala Pro Ala Trp Leu Ser Met Gly Val
 565 570 575

 tta atg ttg tat acc ttg aca atc agt tgt gta ggg tgg ata ctg aaa 1776
 Leu Met Leu Tyr Thr Leu Thr Ile Ser Cys Val Gly Trp Ile Leu Lys
 580 585 590

 gga cgg agg atc aag ata tag 1797
 Gly Arg Arg Ile Lys Ile
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 <213> Cryptococcus neoformans

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 Thr Tyr Ala Leu Trp Ile Ala Leu Ser Pro Tyr Ile Arg His Gly Leu
 35 40 45

 Leu Asn Asn Tyr Leu Ile Cys Val Leu Pro Leu Leu Phe Gly Val Thr

50																			
Ile	Phe	Ser	Thr	Ser	Pro	Leu	Val	Phe	Thr	Ser	Phe	Leu	Ser	Ile	Ile				
65					70					75					80				
Ser	Leu	Ala	Phe	Ile	Thr	Lys	Ser	Gln	Lys	Cys	Phe	Lys	Ser	Val	Ser				
				85					90					95					
Ser	Pro	Glu	Lys	Pro	Lys	Gly	Gln	Trp	Leu	Asp	Glu	Ser	Asp	Ser	Asp				
			100					105					110						
Glu	Glu	Pro	Ala	Glu	Pro	Ala	Ser	Ala	Ala	Gly	Ser	Ala	Ala	Val	Ser				
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Pro	Val	Lys	Leu	Leu	Pro	Ser	Gln	Val	Ala	Phe	Ala	Ser	Gly	Ser	Leu				
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Leu	Ser	Pro	Asp	Pro	Thr	Thr	Ser	Pro	Met	Ser	Pro	Ser	Ser	Ser	Ser				
145					150					155					160				
Ala	Ser	Gly	His	Glu	Asp	Pro	Leu	Gly	Ile	Met	Gly	Val	Asn	Arg	Arg				
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Arg	Ser	Leu	Leu	Glu	Gly	Val	Ser	Leu	Asp	Val	Pro	Ser	His	Ile	Asp				
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Ser	Lys	Val	Arg	Ile	Ser	Pro	Val	Pro	Tyr	Leu	Arg	Leu	Lys	Lys	Ser				
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Arg	Ala	Thr	Lys	Ala	Gln	Trp	Val	Lys	Glu	Lys	Gly	Arg	Leu	Pro	Phe				
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Leu	Thr	Val	Tyr	Arg	Ala	His	Met	Met	Leu	Met	Thr	Val	Ile	Cys	Ile				
225					230					235					240				
Leu	Ala	Val	Asp	Phe	Glu	Val	Phe	Pro	Arg	Trp	Gln	Gly	Lys	Cys	Glu				
				245					250					255					
Asp	Phe	Gly	Thr	Ser	Leu	Met	Asp	Val	Gly	Val	Gly	Ser	Phe	Val	Phe				
			260					265					270						
Ser	Leu	Gly	Leu	Val	Ser	Thr	Lys	Ser	Leu	Ser	Pro	Pro	Pro	Pro	Thr				
			275				280					285							
Pro	Thr	Pro	Ser	Ser	Pro	Ala	Leu	Asn	Ser	His	Ile	Ile	Pro	Leu	Thr				
			290			295					300								
Pro	Ser	Pro	Phe	Thr	Ser	Ile	Leu	Ile	Ser	Leu	Arg	Lys	Ser	Ile	Pro				
305					310					315				320					
Ile	Leu	Val	Leu	Gly	Phe	Ile	Arg	Leu	Ile	Met	Val	Lys	Gly	Ser	Asp				
				325					330					335					

Tyr Pro Glu His Val Thr Glu Tyr Gly Val His Trp Asn Phe Phe Phe
 340 345 350
 Thr Leu Ala Leu Val Pro Val Leu Ala Val Gly Ile Arg Pro Leu Thr
 355 360 365
 Gln Trp Leu Arg Trp Ser Val Leu Gly Val Ile Ile Ser Leu Leu His
 370 375 380
 Gln Leu Trp Leu Thr Tyr Tyr Leu Gln Ser Ile Val Phe Ser Phe Gly
 385 390 395 400
 Arg Ser Gly Ile Phe Leu Ala Asn Lys Glu Gly Phe Ser Ser Leu Pro
 405 410 415
 Gly Tyr Leu Ser Ile Phe Leu Ile Gly Leu Ser Ile Gly Asp His Val
 420 425 430
 Leu Arg Leu Ser Leu Pro Pro Arg Arg Glu Arg Val Val Ser Glu Thr
 435 440 445
 Asn Glu Glu His Glu Gln Ser His Phe Glu Arg Lys Lys Leu Asp Leu
 450 455 460
 Ile Met Glu Leu Ile Gly Tyr Ser Leu Gly Trp Trp Ala Leu Leu Gly
 465 470 475 480
 Gly Trp Ile Trp Ala Gly Gly Glu Val Ser Arg Arg Leu Ala Asn Ala
 485 490 495
 Pro Tyr Val Phe Trp Val Ala Ala Tyr Asn Thr Thr Phe Leu Leu Gly
 500 505 510
 Tyr Leu Leu Leu Thr His Ile Ile Pro Ser Pro Thr Ser Ser Gln Thr
 515 520 525
 Ser Pro Ser Ile Leu Val Pro Pro Leu Leu Asp Ala Met Asn Lys Asn
 530 535 540
 Gly Leu Ala Ile Phe Leu Ala Ala Asn Leu Leu Thr Gly Leu Val Asn
 545 550 555 560
 Val Ser Met Lys Thr Met Tyr Ala Pro Ala Trp Leu Ser Met Gly Val
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 <213> Artificial sequence

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